

L. Helms

1642Helms

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/038,261

DATE: 09/28/1999
TIME: 15:04:12

INPUT SET: S33504.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ATTACHMENT
TO
#11

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5
6 (i) APPLICANT: Reiter, Robert
7 Witte, Owen
8
9 (ii) TITLE OF THE INVENTION: PSCA: Prostate Stem Cell Antigen
10
11
12 (iii) NUMBER OF SEQUENCES: 7
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Mandel & Adriano
16 (B) STREET: 35 N. Arroyo Parkway, Suite 60
17 (C) CITY: Pasadena
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 91103
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/038,261
30 (B) FILING DATE: 10-MAR-1998
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/814,279
35 (B) FILING DATE: 10-MAR-1997
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Sarah B. Adriano
39 (B) REGISTRATION NUMBER: 34,470
40 (C) REFERENCE/DOCKET NUMBER: 30435.54USI2
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 626-395-7801
44 (B) TELEFAX: 626-395-0694
45 (C) TELEX:
46

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47
48         (2) INFORMATION FOR SEQ ID NO:1:
49
50     (i) SEQUENCE CHARACTERISTICS:
51         (A) LENGTH: 998 base pairs
52         (B) TYPE: nucleic acid
53         (C) STRANDEDNESS: single
54         (D) TOPOLOGY: linear
55     (ii) MOLECULE TYPE: cDNA
56     (ix) FEATURE:
57
58         (A) NAME/KEY: Other
59         (B) LOCATION: 1...998
60         (D) OTHER INFORMATION: Human PSCA nucleotide sequence
61
62     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64     AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC      60
65     TGCAGCCAGG CACTGCCCTG CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT      120
66     GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG      180
67     CAGTTGGCCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC      240
68     AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGCTGTGA CACCGACTTG TGCAACGCCA      300
69     GCGGGGCCCC TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCATCGGCC      360
70     TGCTGCTCTG GGGACCCGGC CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCACTG      420
71     GGTGTGGTGC CCCAGGCCTT TGTGCCACTC CTCACAGAAC CTGGCCAGT GGGAGCCTGT      480
72     CCTGGTTCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGCA CCCCTTTTCC      540
73     CCNAACCCTG ACCTTCCCAT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTTAG      600
74     TGANACANAT CCGCNTGCAG ATGGCCCTC CAACNNTTIN TGTTGNTGTT TCCATGGCCC      660
75     AGCATTTTCC ACCCTTAACC CTGTGTTTCTG CACTTNTTTC CCCCAGGAAG CTTTCCCTGC      720
76     CCACCCCAT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG      780
77     ACAGGCAATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG      840
78     ACAAGAGTTG ACGTGAGTTC CTGGGAGTTT CCAGAGATGG GGCCTGGAGG CCTGGAGGAA      900
79     GGGGCCAGGC CTCACATTG TGGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT      960
80     TAATAAACAC CTGTTGGATA AGCCAAAAA AAAAAAAA      998
81
82         (2) INFORMATION FOR SEQ ID NO:2:
83
84     (i) SEQUENCE CHARACTERISTICS:
85         (A) LENGTH: 123 amino acids
86         (B) TYPE: amino acid
87         (C) STRANDEDNESS: unknown
88         (D) TOPOLOGY: unknown
89     (ii) MOLECULE TYPE: protein
90     (ix) FEATURE:
91
92         (A) NAME/KEY: Other
93         (B) LOCATION: 1...123
94         (D) OTHER INFORMATION: Human PSCA amino acid sequence
95
96     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
97
98     Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
99     1           5           10          15

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100 Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
101 20 25 30
102 Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
103 35 40 45
104 Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
105 50 55 60
106 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
107 65 70 75 80
108 Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
109 85 90 95
110 Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
111 100 105 110
112 Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
113 115 120
114

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...441

(D) OTHER INFORMATION: mPSCA nucleotide sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

131 ATGAAGACAG TTTT TTTTAT CCTGCTGGCC ACCTACTTAG CCCTGCATCC AGGTGCTGCT 60
132 CTGCAGTGCT ATTCATGCAC AGCACAGATG AACAAACAGAG ACTGTCTGAA TGTACAGAAC 120
133 TGCAGCCTGG ACCAGCACAG TTGCTTTACA TCGCGCATCC GGGCCATTGG ACTCGTGACA 180
134 GTTATCAGTA AGGGCTGCAG CTCACAGTGT GAGGATGACT CGGAGAACTA CTATTTGGGC 240
135 AAGAAGAACA TCACGTGCTG CTA CTCTGAC CTGTGCAATG TCAACGGGGC CCACACCCTG 300
136 AAGCCACCCA CCACCCTGGG GCTGCTGACC GTGCTCTGCA GCCTGTTGCT GTGGGGCTCC 360
137 AGCCGTCTGT AGGCTCTGGG AGAGCCTACC ATAGCCCGAT TGTGAAGGGA TGAGCTGCAC 420
138 TCCACCCAC CCCCACACAG G 441
139

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...123

(D) OTHER INFORMATION: mPSCA amino acid translation

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153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
154
155 Met Lys Thr Val Phe Phe Ile Leu Leu Ala Thr Tyr Leu Ala Leu His
156 1 5 10 15
157 Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn
158 20 25 30
159 Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys
160 35 40 45
161 Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys
162 50 55 60
163 Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly
164 65 70 75 80
165 Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly
166 85 90 95
167 Ala His Thr Leu Lys Pro Pro Thr Thr Leu Gly Leu Leu Thr Val Leu
168 100 105 110
169 Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu
170 115 120
171

172 (2) INFORMATION FOR SEQ ID NO:5:
173

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 140 amino acids

176 (B) TYPE: amino acid

177 (C) STRANDEDNESS: unknown

178 (D) TOPOLOGY: unknown

179 (ix) FEATURE:
180

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
182

183 Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu
184 1 5 10 15
185 Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn
186 20 25 30
187 Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys
188 35 40 45
189 Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly
190 50 55 60
191 His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly
192 65 70 75 80
193 Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe
194 85 90 95
195 Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr
196 100 105 110
197 Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Leu Pro Ala Leu Leu Arg
198 115 120 125
199 Phe Gly Pro Leu Leu Leu Trp Gly Pro Gly Gln Leu
200 130 135 140
201

202 (2) INFORMATION FOR SEQ ID NO:6:
203

204 (i) SEQUENCE CHARACTERISTICS:

205 (A) LENGTH: 123 amino acids

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206          (B) TYPE: amino acid
207          (C) STRANDEDNESS: unknown
208          (D) TOPOLOGY: unknown
209
210          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
211
212  Met  Lys  Ala  Val  Leu  Leu  Ala  Leu  Leu  Met  Ala  Gly  Leu  Ala  Leu  Gln
213    1      5      10      15
214  Pro  Gly  Thr  Ala  Leu  Leu  Cys  Tyr  Ser  Cys  Lys  Ala  Gln  Val  Ser  Asn
215      20      25      30
216  Glu  Asp  Cys  Leu  Gln  Val  Glu  Asn  Cys  Thr  Gln  Leu  Gly  Glu  Gln  Cys
217      35      40      45
218  Trp  Thr  Ala  Arg  Ile  Arg  Ala  Val  Gly  Leu  Leu  Thr  Val  Ile  Ser  Lys
219      50      55      60
220  Gly  Cys  Ser  Leu  Asn  Cys  Val  Asp  Asp  Ser  Gln  Asp  Tyr  Tyr  Val  Gly
221      65      70      75      80
222  Lys  Lys  Asn  Ile  Thr  Cys  Cys  Asp  Thr  Asp  Leu  Cys  Asn  Ala  Ser  Gly
223      85      90      95
224  Ala  His  Ala  Leu  Gln  Pro  Ala  Ala  Ala  Ile  Leu  Ala  Leu  Leu  Pro  Ala
225      100     105     110
226  Leu  Gly  Leu  Leu  Leu  Trp  Gly  Pro  Gly  Gln  Leu
227      115     120
228
229          (2) INFORMATION FOR SEQ ID NO:7:
230
231          (i) SEQUENCE CHARACTERISTICS:
232              (A) LENGTH: 123 amino acids
233              (B) TYPE: amino acid
234              (C) STRANDEDNESS: unknown
235              (D) TOPOLOGY: unknown
236
237          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
238
239  Met  Lys  Thr  Val  Leu  Phe  Leu  Leu  Leu  Ala  Thr  Tyr  Leu  Ala  Leu  His
240    1      5      10      15
241  Pro  Gly  Ala  Ala  Leu  Gln  Cys  Tyr  Ser  Cys  Thr  Ala  Gln  Met  Asn  Asn
242      20      25      30
243  Arg  Asp  Cys  Leu  Asn  Val  Gln  Asn  Cys  Ser  Leu  Asp  Gln  His  Ser  Cys
244      35      40      45
245  Phe  Thr  Ser  Arg  Ile  Arg  Ala  Ile  Gly  Leu  Val  Thr  Val  Ile  Ser  Lys
246      50      55      60
247  Gly  Cys  Ser  Ser  Gln  Cys  Glu  Asp  Asp  Ser  Glu  Asn  Tyr  Tyr  Leu  Gly
248      65      70      75      80
249  Lys  Lys  Asn  Ile  Thr  Cys  Cys  Tyr  Ser  Asp  Leu  Cys  Asn  Val  Asn  Gly
250      85      90      95
251

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text